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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/183,972A

 DATE: 05/08/2000
 TIME: 20:30:47

Input Set: I183972A.RAW

This Raw Listing contains the General Information
 Section and up to first 5 pages.

1 <110> APPLICANT: Hageman, Gregory S.
 2 Kuehn, Markus H.
 3 <120> TITLE OF INVENTION: THERAPEUTICS AND DIAGNOSTICS FOR OCULAR DISEASE BASED
 4 ON A NOVEL HUMAN GENE FAMILY
 5 <130> FILE REFERENCE: UIA-027.01
 6 <140> CURRENT APPLICATION NUMBER: US/09/183,972A
 7 <141> CURRENT FILING DATE: 1998-10-29
 8 <160> NUMBER OF SEQ ID NOS: 49
 9 <170> SOFTWARE: PatentIn Ver. 2.0
 10 <210> SEQ ID NO 1
 11 <211> LENGTH: 555
 12 <212> TYPE: DNA
 13 <213> ORGANISM: Callimico sp.
 14 <220> FEATURE:
 15 <221> NAME/KEY: CDS
 16 <222> LOCATION: (1)..(555)
 17 <400> SEQUENCE: 1

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20	1 5 10 15	
21	cag att tta gcc agt ctt caa gct tat tat aga ttg aga gtg tgt cag	96
22	Gln Ile Leu Ala Ser Leu Gln Ala Tyr Tyr Arg Leu Arg Val Cys Gln	
23	20 25 30	
24	gaa gca gta tgg gaa gca tat cgg atc ttt ctg gat cgc atc cct gac	144
25	Glu Ala Val Trp Glu Ala Tyr Arg Ile Phe Leu Asp Arg Ile Pro Asp	
26	35 40 45	
27	aca ggg gaa tat cag gac tgg gtc agc ttc tgc cag cag gag acc ttc	192
28	Thr Gly Glu Tyr Gln Asp Trp Val Ser Phe Cys Gln Gln Glu Thr Phe	
29	50 55 60	
30	tgc ctc ttt gac atc gga caa aac ttc agc aat tcc cag gag cac ctg	240
31	Cys Leu Phe Asp Ile Gly Gln Asn Phe Ser Asn Ser Gln Glu His Leu	
32	65 70 75 80	
33	gat ctt ctc cag cag aga ata aaa cag aga agt ttc cct gag aga aaa	288
34	Asp Leu Leu Gln Gln Arg Ile Lys Gln Arg Ser Phe Pro Glu Arg Lys	
35	85 90 95	
36	gat gaa gta tct aca gag aag aca ttg gga gag cct agt gaa acc att	336
37	Asp Glu Val Ser Thr Glu Lys Thr Leu Gly Glu Pro Ser Glu Thr Ile	
38	100 105 110	
39	gtg gtt tca aca gat gtt gcc agc gtc tca ctt ggg cct ttc cct gtc	384
40	Val Val Ser Thr Asp Val Ala Ser Val Ser Leu Gly Pro Phe Pro Val	
41	115 120 125	
42	act cct gat gac acc ctc ctc aat gaa att ctc gat aat gca ctc aac	432
43	Thr Pro Asp Asp Thr Leu Leu Asn Glu Ile Leu Asp Asn Ala Leu Asn	
44	130 135 140	

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45      gac acc aag atg cct aca aca gaa aga gaa aca gaa ctc gct gtg tct      480
46      Asp Thr Lys Met Pro Thr Thr Glu Arg Glu Thr Glu Leu Ala Val Ser
47      145                      150                      155                      160
48      gag gag cag agg gtg gag ctc agc atc tct ctg ata aac cag agg ttc      528
49      Glu Glu Gln Arg Val Glu Leu Ser Ile Ser Leu Ile Asn Gln Arg Phe
50                      165                      170                      175
51      aag gca gag ctc gct gac tct cag tca                                555
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56      <212> TYPE: PRT
57      <213> ORGANISM: Callimico sp.
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62                      20                      25                      30
63      Glu Ala Val Trp Glu Ala Tyr Arg Ile Phe Leu Asp Arg Ile Pro Asp
64                      35                      40                      45
65      Thr Gly Glu Tyr Gln Asp Trp Val Ser Phe Cys Gln Gln Glu Thr Phe
66                      50                      55                      60
67      Cys Leu Phe Asp Ile Gly Gln Asn Phe Ser Asn Ser Gln Glu His Leu
68                      65                      70                      75                      80
69      Asp Leu Leu Gln Gln Arg Ile Lys Gln Arg Ser Phe Pro Glu Arg Lys
70                      85                      90                      95
71      Asp Glu Val Ser Thr Glu Lys Thr Leu Gly Glu Pro Ser Glu Thr Ile
72                      100                     105                     110
73      Val Val Ser Thr Asp Val Ala Ser Val Ser Leu Gly Pro Phe Pro Val
74                      115                     120                     125
75      Thr Pro Asp Asp Thr Leu Leu Asn Glu Ile Leu Asp Asn Ala Leu Asn
76                      130                     135                     140
77      Asp Thr Lys Met Pro Thr Thr Glu Arg Glu Thr Glu Leu Ala Val Ser
78      145                      150                      155                      160
79      Glu Glu Gln Arg Val Glu Leu Ser Ile Ser Leu Ile Asn Gln Arg Phe
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83      <210> SEQ ID NO 3
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87      <220> FEATURE:
88      <221> NAME/KEY: CDS
89      <222> LOCATION: (128)..(2440)
90      <220> FEATURE:
91      <223> OTHER INFORMATION: "n" bases at various positions throughout the sequence
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94      taaaccaaga aggttatcct caatcatctg gtatcaatat ataattattt ttcctttntg 60

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W-->

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95	ttacttttta atgagatttg aggttggttct gtgattgtta tcagaattac catgcacaaa	120
96	agccaga atg tat ttg gaa act aga aga gct att ttt gtt ttt tgg att	169
97	Met Tyr Leu Glu Thr Arg Arg Ala Ile Phe Val Phe Trp Ile	
98	1 5 10	
99	ttt ctc caa gtt caa gga act aaa gat atc tcc att aac ata tac cat	217
100	Phe Leu Gln Val Gln Gly Thr Lys Asp Ile Ser Ile Asn Ile Tyr His	
101	15 20 25 30	
102	tct gaa act aaa gac ata gac aat ccc cca aga aat gaa aca act gaa	265
103	Ser Glu Thr Lys Asp Ile Asp Asn Pro Pro Arg Asn Glu Thr Thr Glu	
104	35 40 45	
105	agt act gaa aaa atg tac aaa atg tca act atg aga cga ata ttc gat	313
106	Ser Thr Glu Lys Met Tyr Lys Met Ser Thr Met Arg Arg Ile Phe Asp	
107	50 55 60	
108	ttg gca aag cat cga aca aaa aga tcc gca ttt ttc cca acg ggg gtt	361
109	Leu Ala Lys His Arg Thr Lys Arg Ser Ala Phe Phe Pro Thr Gly Val	
110	65 70 75	
111	aaa gtc tgt cca cag gaa tcc atg aaa cag att tta gac agt ctt caa	409
112	Lys Val Cys Pro Gln Glu Ser Met Lys Gln Ile Leu Asp Ser Leu Gln	
113	80 85 90	
114	gct tat tat aga ttg aga gtg tgt cag gaa gca gta tgg gaa gca tat	457
115	Ala Tyr Tyr Arg Leu Arg Val Cys Gln Glu Ala Val Trp Glu Ala Tyr	
116	95 100 105 110	
117	cgg atc ttt ctg gat cgc atc cct gac aca ggg gaa tat cag gac tgg	505
118	Arg Ile Phe Leu Asp Arg Ile Pro Asp Thr Gly Glu Tyr Gln Asp Trp	
119	115 120 125	
120	gtc agc atc tgc cag cag gag acc ttc tgc ctc ttt gac att gga aaa	553
121	Val Ser Ile Cys Gln Gln Glu Thr Phe Cys Leu Phe Asp Ile Gly Lys	
122	130 135 140	
123	aac ttc agc aat tcc cag gag cac ctg gat ctt ctc cag cag aga ata	601
124	Asn Phe Ser Asn Ser Gln Glu His Leu Asp Leu Leu Gln Gln Arg Ile	
125	145 150 155	
126	aaa cag aga agt ttc cct gac aga aaa gat gaa ata tct gca gag aag	649
127	Lys Gln Arg Ser Phe Pro Asp Arg Lys Asp Glu Ile Ser Ala Glu Lys	
128	160 165 170	
129	aca ttg gga gag cct ggt gaa acc att gtc att tca aca gat gtt gcc	697
130	Thr Leu Gly Glu Pro Gly Glu Thr Ile Val Ile Ser Thr Asp Val Ala	
131	175 180 185 190	
132	aac gtc tca ctt ggg cct ttc cct ctc act cct gat gac acc ctc ctc	745
133	Asn Val Ser Leu Gly Pro Phe Pro Leu Thr Pro Asp Asp Thr Leu Leu	
134	195 200 205	
135	aat gaa att ctc gat aat aca ctc aac gac acc aag atg cct aca aca	793
136	Asn Glu Ile Leu Asp Asn Thr Leu Asn Asp Thr Lys Met Pro Thr Thr	
137	210 215 220	
138	gaa aga gaa aca gaa ttc gct gtg ttg gag gag cag agg gtg gag ctc	841
139	Glu Arg Glu Thr Glu Phe Ala Val Leu Glu Glu Gln Arg Val Glu Leu	
140	225 230 235	
141	agc gtc tct ctg gta aac cag aag ttc aag gca gag ctc gct gac tcc	889
142	Ser Val Ser Leu Val Asn Gln Lys Phe Lys Ala Glu Leu Ala Asp Ser	
143	240 245 250	
144	cag tcc cca tat tac cag gag cta gca gga aag tcc caa ctt cag atg	937

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145	Gln Ser Pro Tyr Tyr Gln Glu Leu Ala Gly Lys Ser Gln Leu Gln Met	
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147	caa aag ata ttt aag aaa ctt cca gga ttc aaa aaa atc cat gtg tta	985
148	Gln Lys Ile Phe Lys Lys Leu Pro Gly Phe Lys Lys Ile His Val Leu	
149	275 280 285	
150	gga ttt aga cca aag aaa gaa aaa gat ggc tca agc tcc aca gag atg	1033
151	Gly Phe Arg Pro Lys Lys Glu Lys Asp Gly Ser Ser Ser Thr Glu Met	
152	290 295 300	
153	caa ctt acg gcc atc ttt aag aga cac agt gca gaa gca aaa agc cct	1081
154	Gln Leu Thr Ala Ile Phe Lys Arg His Ser Ala Glu Ala Lys Ser Pro	
155	305 310 315	
156	gca agt gac ctc ctg tct ttt gat tcc aac aaa att gaa agt gag gaa	1129
157	Ala Ser Asp Leu Leu Ser Phe Asp Ser Asn Lys Ile Glu Ser Glu Glu	
158	320 325 330	
159	gtc tat cat gga acc atg gag gag gac aag caa cca gaa atc tat ctc	1177
160	Val Tyr His Gly Thr Met Glu Glu Asp Lys Gln Pro Glu Ile Tyr Leu	
161	335 340 345 350	
162	aca gct aca gac ctc aaa agg ctg atc agc aaa gca cta gag gaa gaa	1225
163	Thr Ala Thr Asp Leu Lys Arg Leu Ile Ser Lys Ala Leu Glu Glu Glu	
164	355 360 365	
165	caa tct ttg gat gtg ggg aca att cag ttc act gat gaa att gct gga	1273
166	Gln Ser Leu Asp Val Gly Thr Ile Gln Phe Thr Asp Glu Ile Ala Gly	
167	370 375 380	
168	tca ctg cca gcc ttt ggt cct gac acc caa tca gag ctg ccc aca tct	1321
169	Ser Leu Pro Ala Phe Gly Pro Asp Thr Gln Ser Glu Leu Pro Thr Ser	
170	385 390 395	
171	ttt gct gtt ata aca gag gat gct act ttg agt cca gaa ctt cct cct	1369
172	Phe Ala Val Ile Thr Glu Asp Ala Thr Leu Ser Pro Glu Leu Pro Pro	
173	400 405 410	
174	gtt gaa ccc cag ctt gag aca gtg gac gga gca gag cat ggt cta cct	1417
175	Val Glu Pro Gln Leu Glu Thr Val Asp Gly Ala Glu His Gly Leu Pro	
176	415 420 425 430	
177	gac act tct tgg tct cca cct gct atg gcc tct acc tcc ctg tca gaa	1465
178	Asp Thr Ser Trp Ser Pro Pro Ala Met Ala Ser Thr Ser Leu Ser Glu	
179	435 440 445	
180	gct cca cct ttc ttt atg gca tca agc atc ttc tct ctg act gat caa	1513
181	Ala Pro Pro Phe Phe Met Ala Ser Ser Ile Phe Ser Leu Thr Asp Gln	
182	450 455 460	
183	ggc acc aca gat aca atg gcc act gac cag aca atg cta gta cca ggg	1561
184	Gly Thr Thr Asp Thr Met Ala Thr Asp Gln Thr Met Leu Val Pro Gly	
185	465 470 475	
186	ctc acc atc ccc acc agt gat tat tct gca atc agc caa ctg gct ctg	1609
187	Leu Thr Ile Pro Thr Ser Asp Tyr Ser Ala Ile Ser Gln Leu Ala Leu	
188	480 485 490	
189	gga att tca cat cca cct gca tct tca gat gac agc cga tca agt gca	1657
190	Gly Ile Ser His Pro Pro Ala Ser Ser Asp Asp Ser Arg Ser Ser Ala	
191	495 500 505 510	
192	ggg ggc gaa gat atg gtc aga cac cta gat gaa atg gat ctg tct gac	1705
193	Gly Gly Glu Asp Met Val Arg His Leu Asp Glu Met Asp Leu Ser Asp	
194	515 520 525	

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 DATE: 05/08/2000
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Input Set: I183972A.RAW

195	act cct gcc cca tct gag gta cca gag ctc agc gaa tat gtt tct gtc	1753
196	Thr Pro Ala Pro Ser Glu Val Pro Glu Leu Ser Glu Tyr Val Ser Val	
197	530 535 540	
198	cca gat cat ttc ttg gag gat acc act cct gtc tca gct tta cag tat	1801
199	Pro Asp His Phe Leu Glu Asp Thr Thr Pro Val Ser Ala Leu Gln Tyr	
200	545 550 555	
201	atc acc act agt tct atg acc att gcc ccc aag ggc cga gag ctg gta	1849
202	Ile Thr Thr Ser Ser Met Thr Ile Ala Pro Lys Gly Arg Glu Leu Val	
203	560 565 570	
204	gtg ttc ttc agt ctg cgt gtt gct aac atg gcc ttc tcc aac gac ctg	1897
205	Val Phe Phe Ser Leu Arg Val Ala Asn Met Ala Phe Ser Asn Asp Leu	
206	575 580 585 590	
207	ttc aac aag agc tct ctg gag tac cga gct ctg gag caa caa ttc aca	1945
208	Phe Asn Lys Ser Ser Leu Glu Tyr Arg Ala Leu Glu Gln Gln Phe Thr	
209	595 600 605	
210	cag ctg ctg gtt cca tat cta cga tcc aat ctt aca gga ttt aag caa	1993
211	Gln Leu Leu Val Pro Tyr Leu Arg Ser Asn Leu Thr Gly Phe Lys Gln	
212	610 615 620	
213	ctt gaa ata ctt aac ttc aga aac ggg agt gtg att gtg aat agc aaa	2041
214	Leu Glu Ile Leu Asn Phe Arg Asn Gly Ser Val Ile Val Asn Ser Lys	
215	625 630 635	
216	atg aag ttt gct aag tct gtg ccg tat aac ctc acc aag gct gtg cac	2089
217	Met Lys Phe Ala Lys Ser Val Pro Tyr Asn Leu Thr Lys Ala Val His	
218	640 645 650	
219	ggg gtc ttg gag gat ttt cgt tct gct gca gcc caa caa ctc cat ctg	2137
220	Gly Val Leu Glu Asp Phe Arg Ser Ala Ala Ala Gln Gln Leu His Leu	
221	655 660 665 670	
222	gaa ata gac agc tac tct ctc aac att gaa cca gct gat caa gca gat	2185
223	Glu Ile Asp Ser Tyr Ser Leu Asn Ile Glu Pro Ala Asp Gln Ala Asp	
224	675 680 685	
225	ccc tgc aag ttc ctg gcc tgc ggc gaa ttt gcc caa tgt gta aag aac	2233
226	Pro Cys Lys Phe Leu Ala Cys Gly Glu Phe Ala Gln Cys Val Lys Asn	
227	690 695 700	
228	gaa cgg act gag gaa gcg gag tgt cgc tgc aaa cca gga tat gac agc	2281
229	Glu Arg Thr Glu Glu Ala Glu Cys Arg Cys Lys Pro Gly Tyr Asp Ser	
230	705 710 715	
231	cag ggg agc ctg gac ggt ctg gaa cca ggc ctc tgt ggc ctg gca caa	2329
232	Gln Gly Ser Leu Asp Gly Leu Glu Pro Gly Leu Cys Gly Leu Ala Gln	
233	720 725 730	
234	agg aat gcg agg tcc tcc agg gaa agg gag ctc cat gcg gtt cca gat	2377
235	Arg Asn Ala Arg Ser Ser Arg Glu Arg Glu Leu His Ala Val Pro Asp	
236	735 740 745 750	
237	cac tct gaa aat caa gca tac aaa act agt gtt aaa agt tcc aaa atc	2425
238	His Ser Glu Asn Gln Ala Tyr Lys Thr Ser Val Lys Ser Ser Lys Ile	
239	755 760 765	
240	aac aaa ata aca agg taatcagtaa aagaaattct gaattactga ccgtagaata	2480
241	Asn Lys Ile Thr Arg	
242	770	
243	tgaagaattt aaccatcaag attgggaagg aaattaaaaa ctgaaaatgt acaattatca	2540
244	cttaggctat ctcaagagag atgatttgcc ttctcaagga aaatggagac aggcatattc	2600

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I183972A.RAW

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612	W "N" or "Xaa" used: Feature required	atagggcaca ctgttttttt ttcagcttaa gntttcag
798	W "N" or "Xaa" used: Feature required	Xaa Val Phe Phe Pro Thr Gly Val Lys Val X
811	W "N" or "Xaa" used: Feature required	Xaa Val Leu Phe Pro Asn Gly Val Lys Ile
824	W "N" or "Xaa" used: Feature required	tattaggaat tccatytttyt tyccnaaygg
836	W "N" or "Xaa" used: Feature required	ttncnngcna gytcytgrta rtangg
1126	W "N" or "Xaa" used: Feature required	Xaa Ala Leu Phe Pro Asn Gly Val Leu Ile X
1145	W "N" or "Xaa" used: Feature required	Xaa Ile Leu Phe Pro Asn Gly Val Leu Ile X
1170	W "N" or "Xaa" used: Feature required	Xaa Ile Phe Phe Pro Thr Gly Val Lys Val X